STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/564,484_

Source: _IFWP_

Date Processed by STIC: _1/20/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/564,484_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length
The rules require that a line **not exceed 72** characters in length. This includes white spaces.

3____Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4____Non-ASCII
The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5____Variable Length
Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10____Invalid <213>
Response
Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11____Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa
"n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

IFWP

RAW SEQUENCE LISTING   DATE: 01/20/2006
PATENT APPLICATION: US/10/564,484   TIME: 12:30:46

Input Set : N:\SMITH\pto.ts20..txt
Output Set: N:\CRF4\01202006\J564484.raw

```
      3 <110> APPLICANT: Japan Science and Technology Corporation
      5 <120> TITLE OF INVENTION: Diagnosis method of endometriosis
      7 <130> FILE REFERENCE: 03-F-104PCT
C-->  9 <140> CURRENT APPLICATION NUMBER: US/10/564,484
C-->  9 <141> CURRENT FILING DATE: 2006-01-13
      9 <150> PRIOR APPLICATION NUMBER: JP2003-196459
     10 <151> PRIOR FILING DATE: 2003-07-14
     12 <160> NUMBER OF SEQ ID NOS: 10
     14 <170> SOFTWARE: PatentIn version 3.1
```

see item 4
on Error Summary
Sheet

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
    177 <210> SEQ ID NO: 8
    178 <211> LENGTH: (22) 29 Shown below
    179 <212> TYPE: DNA
    180 <213> ORGANISM: Artificial
    182 <220> FEATURE:
    183 <223> OTHER INFORMATION: Description of Artificial sequence: Synthetic
oligonucleotide
    185 <400> SEQUENCE: 8
E--> 186 ttgaattctt aacatttctc catctctaa                              29
    201 <210> SEQ ID NO: 10
    202 <211> LENGTH: 28
    203 <212> TYPE: DNA
    204 <213> ORGANISM: Artificial
    206 <220> FEATURE:
    207 <223> OTHER INFORMATION: Description of Artificial sequence: Synthetic
oligonucleotide
    209 <400> SEQUENCE: 10
    210 ggccgaattc agatccaaaa taattgcc                                 28
E--> 211 (1/5)
```

delete

VERIFICATION SUMMARY   DATE: 01/20/2006
PATENT APPLICATION: **US/10/564,484**   TIME: 12:30:47

Input Set : **N:\SMITH\pto.ts20..txt**
Output Set: **N:\CRF4\01202006\J564484.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:26 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:24
L:186 M:252 E: No. of Seq. differs, <211> LENGTH:Input:22 Found:29 SEQ:8
L:211 M:254 E: No. of Bases conflict, LENGTH:Input:5 Counted:29 SEQ:10
L:211 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:211 M:252 E: No. of Seq. differs, <211> LENGTH:Input:28 Found:29 SEQ:10